

## Executive Summary

# Resistance and Pathogenicity of *Salmonella* Thompson

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*Salmonella* non-typhoid (NTS), a zoonotic foodborne pathogen with flagella that causes systemic infections in poultry and acute gastroenteritis in humans, costs poultry farms a lot of money. The tools of *Salmonella* surveillance have quickly increased with the advancement of sequencing technologies. Due to its capacity to gather complete and detailed genetic data of a species, whole-genome sequencing (WGS) has recently supplanted conventional molecular techniques like pulsed-field gel electrophoresis (PFGE) as a novel method to track the spread of bacterial infectious illnesses. Therefore, the purpose of this work was to investigate the pathogenicity and antibiotic resistance of clinical *S. Thompson* isolated from dead chicken embryos.

384 suspected *Salmonella* isolates covering the stages of incubation, breeding, processing, and circulation were gathered from Shandong Province and Beijing, China, during the surveillance of *Salmonella*. Raw chicken flesh, chicks, and chicken embryos were among the samples gathered. A commercial *Salmonella* biochemical assay was used to identify the purified *Salmonella* isolates. Every day at the same time, faeces of the same quality were collected from each group to measure the amount of *Salmonella* in the faeces and identify the species.

The isolates from dead poultry embryos at the poultry farm's incubation end gave us the chance to systematically research pathogenic avian *S. Thompson* for this investigation.

Because just one serotype of *Salmonella* was found in the yolk sac and this batch of eggs in the broiler breeding farm had a 25% hatching mortality rate, it is most likely that *S. Thompson* was to blame for the sharp decline in the rate of successful hatching. The identification of the strain was followed by an evolutionary investigation. Analysis of the evolutionary relationship of 16S rRNA genes alone is restricted due to the discrepancy between the evolutionary rate of genes and that of the species.

Both genotyping and phenotyping were done to study antibiotic resistance. The antimicrobial resistance phenotype of bacteria can be predicted by resistance genes, and numerous studies have shown a correlation between the antimicrobial resistance phenotype of bacteria and the results of WGS-based bacterial resistance prediction. *Salmonella*'s virulence is influenced by virulence plasmids, pili, flagella, enterotoxin, and other elements. The crucial SPIs are SPI-1 through SPI-5, which encode the type III secretion system, the killing effect of bacterial escape from macrophages, the survival of *Salmonella* in host macrophages, a type I secretion system, intestinal mucosal fluid secretion, and an inflammatory response, respectively. SPI is involved in the invasion of intestinal epithelial cells.



Conclusion: S. Thompson, which was in fact very pathogenic to young chickens, was the reason for the noticeably lower embryo hatching rate on this farm. The fact that 14 clinical S. Thompson strains likely descended from the same clone, the discovery of the colistin (polymyxin B) resistance gene mcr-9 in S. Thompson, and the identical cgST-12774 typing of S. Thompson of human and avian origin in China all point to the need for improved food hygiene and safety as well as a more precise typing and monitoring system for Salmonella.

Source: [Veterinary Sciences](#)

#### **KEYWORDS**

Salmonella Thompson; cgMLST; mcr-9; antibiotic resistance; chicks

